Name: Santos, Tristan Neal U. Course and Section: CPE32S9 Date of Submission: 02-07-2024 Instructor: Engr. Roman Richard

Part 1, Step 1:

from google.colab import drive
drive.mount('/content/drive')

Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True).

#Code Cell 1

import pandas as pd
brainFile = '/content/drive/MyDrive/Colab
brainFrame = pd.read_csv(brainFile, '\t')
Notebooks/Emtech2/Text/brainsize.txt'

<ipython-input-20-b496ce176638>:4: FutureWarning: In a future version of pandas all arguments of read_csv except for the argument 'filepath_or_buffer' will be keyword-only.
brainFrame = pd.read_csv(brainFile, '\t')

Step 2

#Code Cell 2
brainFrame.head()

	Gender	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
0	Female	133	132	124	118.0	64.5	816932
1	Male	140	150	124	NaN	72.5	1001121
2	Male	139	123	150	143.0	73.3	1038437
3	Male	133	129	128	172.0	68.8	965353
4	Female	137	132	134	147.0	65.0	951545

Part 2, Step 1:

#Code Cell 3

brainFrame.describe()

	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
count	40.000000	40.000000	40.00000	38.000000	39.000000	4.000000e+01
mean	113.450000	112.350000	111.02500	151.052632	68.525641	9.087550e+05
std	24.082071	23.616107	22.47105	23.478509	3.994649	7.228205e+04
min	77.000000	71.000000	72.00000	106.000000	62.000000	7.906190e+05
25%	89.750000	90.000000	88.25000	135.250000	66.000000	8.559185e+05
50%	116.500000	113.000000	115.00000	146.500000	68.000000	9.053990e+05
75%	135.500000	129.750000	128.00000	172.000000	70.500000	9.500780e+05
max	144.000000	150.000000	150.00000	192.000000	77.000000	1.079549e+06

Step 2, A:

#Code Cell 4
import numpy as np
import matplotlib.pyplot as plt

Step 2, B:

#Code Cell 5
menDf = brainFrame[(brainFrame.Gender == 'Male')]
womenDf = brainFrame[(brainFrame.Gender == 'Female')]
womenDf.head()

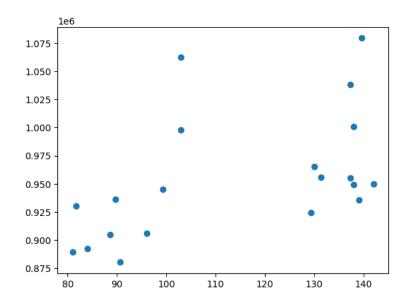
	Gender	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
0	Female	133	132	124	118.0	64.5	816932
4	Female	137	132	134	147.0	65.0	951545
5	Female	99	90	110	146.0	69.0	928799
6	Female	138	136	131	138.0	64.5	991305
7	Female	92	90	98	175.0	66.0	854258

```
#Code Cell 5
menDf = brainFrame[(brainFrame.Gender == 'Male')]
womenDf = brainFrame[(brainFrame.Gender == 'Female')]
menDf.head()
```

	Gender	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
1	Male	140	150	124	NaN	72.5	1001121
2	Male	139	123	150	143.0	73.3	1038437
3	Male	133	129	128	172.0	68.8	965353
8	Male	89	93	84	134.0	66.3	904858
9	Male	133	114	147	172.0	68.8	955466

Step 2, C:

```
# Code cell 6
menMeanSmarts = menDf[["PIQ", "FSIQ", "VIQ"]].mean(axis=1)
plt.scatter(menMeanSmarts, menDf["MRI_Count"])
plt.show()
%matplotlib inline
```



```
# Code cell 7
# Graph the women-only filtered dataframe
#womenMeanSmarts = ?
#plt.scatter(?, ?)
plt.show()
%matplotlib inline
```

Part 3, Step 1:

```
# Code cell 8
brainFrame.corr(method='pearson')
```

<ipython-input-33-cab48f3abe05>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid of brainFrame.corr(method='pearson')

	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
FSIQ	1.000000	0.946639	0.934125	-0.051483	-0.086002	0.357641
VIQ	0.946639	1.000000	0.778135	-0.076088	-0.071068	0.337478
PIQ	0.934125	0.778135	1.000000	0.002512	-0.076723	0.386817
Weight	-0.051483	-0.076088	0.002512	1.000000	0.699614	0.513378
Height	-0.086002	-0.071068	-0.076723	0.699614	1.000000	0.601712
MRI_Count	0.357641	0.337478	0.386817	0.513378	0.601712	1.000000

Code cell 9(Female)
womenDf.corr(method='pearson')

<ipython-input-34-a6271751808a>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid (
womenDf.corr(method='pearson')

	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
FSIQ	1.000000	0.955717	0.939382	0.038192	-0.059011	0.325697
VIQ	0.955717	1.000000	0.802652	-0.021889	-0.146453	0.254933
PIQ	0.939382	0.802652	1.000000	0.113901	-0.001242	0.396157
Weight	0.038192	-0.021889	0.113901	1.000000	0.552357	0.446271
Height	-0.059011	-0.146453	-0.001242	0.552357	1.000000	0.174541
MRI_Count	0.325697	0.254933	0.396157	0.446271	0.174541	1.000000

Code cell 10

Use corr() for the male-only dataframe with the pearson method

#?.corr(?)

Code cell 9(Male)

menDf.corr(method='pearson')

<ipython-input-36-9c6b27fe7b04>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid (
menDf.corr(method='pearson')

	FSIQ	VIQ	PIQ	Weight	Height	MRI_Count
FSIQ	1.000000	0.944400	0.930694	-0.278140	-0.356110	0.498369
VIQ	0.944400	1.000000	0.766021	-0.350453	-0.355588	0.413105
PIQ	0.930694	0.766021	1.000000	-0.156863	-0.287676	0.568237
Weight	-0.278140	-0.350453	-0.156863	1.000000	0.406542	-0.076875
Height	-0.356110	-0.355588	-0.287676	0.406542	1.000000	0.301543
MRI_Count	0.498369	0.413105	0.568237	-0.076875	0.301543	1.000000

Part 4, Step 1:

```
# Code cell 11
!pip install seaborn
```

```
Requirement already satisfied: seaborn in /usr/local/lib/python3.10/dist-packages (0.13.1)

Requirement already satisfied: numpy!=1.24.0,>=1.20 in /usr/local/lib/python3.10/dist-packages (from seaborn) (1.23.5)

Requirement already satisfied: pandas>=1.2 in /usr/local/lib/python3.10/dist-packages (from seaborn) (1.5.3)

Requirement already satisfied: matplotlib!=3.6.1,>=3.4 in /usr/local/lib/python3.10/dist-packages (from seaborn) (3.7.1)

Requirement already satisfied: contourpy>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (1.2.0)

Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (0.12.1)

Requirement already satisfied: fonttools>=4.22.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (4.47.2)

Requirement already satisfied: kiwisolver>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (23.2)

Requirement already satisfied: packaging>=20.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (9.4.0)

Requirement already satisfied: pyparsing>=2.3.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (3.1.1)

Requirement already satisfied: python-dateutil>=2.7 in /usr/local/lib/python3.10/dist-packages (from matplotlib!=3.6.1,>=3.4->seaborn) (2.8.2)

Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dist-packages (from pandas>=1.2->seaborn) (2023.4)

Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.10/dist-packages (from pandas>=1.2->seaborn) (2023.4)
```

```
# Code cell 12
import seaborn as sns
wcorr = womenDf.corr()
sns.heatmap(wcorr)
#plt.savefig('attribute_correlations.png', tight_layout=True)
```

<ipython-input-38-2465c40f5efb>:3: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid (
 wcorr = womenDf.corr()
<Axes: >

Code cell 14
mcorr = menDf.corr()
sns.heatmap(mcorr)
#plt.savefig('attribute_correlations.png', tight_layout=True)

<ipython-input-39-ff3e250059fc>:2: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid (
 mcorr = menDf.corr()

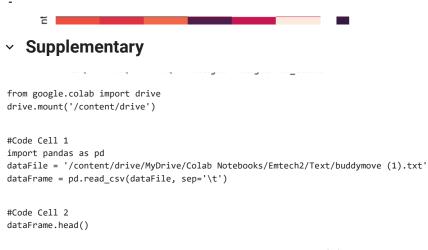
Many variable pairs present correlation close to zero. What does that mean?

-Due to having weak and differential relations towards variable pairs to one another that it feels like theres no difference between them.

Why seperate the Genders?

-To find some differentiation between them while also showcasing what output results we got from them.

What variables have stronger correlation with brain size (MRI_Count)? Is that expected? Explain.



		User Id	Unnamed: 1	Sports	Unnamed: 3	Religious	Nature	Theatre	Shopping	Picnic	Unnamed: 9
User 1	NaN	2	NaN	77	NaN	79	69	68	NaN	95	NaN
User 2	NaN	2	NaN	62	NaN	76	76	69	NaN	68	NaN
User 3	NaN	2	NaN	50	NaN	97	87	50	NaN	75	NaN